

GenCore version 4.5
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OM nucleic - nucleic search, using sw model,

Run on: March 17, 2001, 19:59:58 ; Search time 2564.7 Seconds
(without alignments)
4310.188 Million cell updates/sec

Title: US-09-456-306-1
Perfect score: 2160
Sequence: 1 ttagagggcgaattcgtgag9.....ggtgcccatgagatgcct 2160

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 118133 seqs, 2558875100 residues
Total number of hits satisfying chosen parameters: 2236266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*
1: gb_ba1:*
2: gb_ba2:*
3: gb_om:*
4: gb_ov:*
5: gb_ph:*
6: gb_pl1:*
7: gb_pl2:*
8: gb_pr1:*
9: gb_pr2:*
10: gb_pr3:*
11: gb_to:*
12: gb_sy:*
13: gb_un:*
14: em_fun:*
15: em_hum1:*
16: em_hum2:*
17: em_in:*
18: em_om:*
19: em_or:*
20: em_ov:*
21: em_pat:*
22: em_ph:*
23: em_pl:*
24: em_ro:*
25: em_scs:*
26: em_sy:*
27: em_un:*
28: em_v1:*
29: gb_ds3:*
30: gb_in1:*
31: gb_in2:*
32: gb_in3:*
33: gb_pl3:*
34: gb_pr4:*
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36: em_da2:*
37: em_hc1:*
38: em_hc2:*
39: em_hc3:*
40: em_hc4:*
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46: em_hc10:*
47: em_hum3:*
48: em_hum4:*
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51: gb_pr5:*
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78: gb_hc25:*
79: gb_hc26:*
80: gb_hc27:*
81: gb_hc28:*
82: gb_hc29:*
83: em_hc90:*
84: gb_hc24:*
85: gb_pr8:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1 | 532.4 | 24.6 | 29400 | 29 | SC1A9 |
| 2 | 305.2 | 14.1 | 1974 | 2 | ECPOXB |
| 3 | 305.2 | 14.1 | 11429 | 1 | AE000188 |
| 4 | 305.2 | 14.1 | 19978 | 2 | D90724 |
| 5 | 302 | 14.0 | 1719 | 2 | ECPOXB |
| 6 | 302 | 14.0 | 1719 | 2 | ECOPOR10G |
| 7 | 302 | 14.0 | 1719 | 2 | ECOPOR11G |
| 8 | 302 | 14.0 | 1719 | 2 | ECOPOR12G |
| 9 | 302 | 14.0 | 1719 | 2 | ECOPOR13G |
| 10 | 300.4 | 13.9 | 1719 | 2 | ECOPOR14G |
| 11 | 300.4 | 13.9 | 1719 | 2 | ECOPOR15G |
| 12 | 300.4 | 13.9 | 1719 | 2 | ECOPOR16G |
| 13 | 298.8 | 13.8 | 1719 | 2 | ECOPOR17G |
| 14 | 297.2 | 13.8 | 1440 | 2 | PAORF1 |
| 15 | 289.8 | 13.4 | 10977 | 1 | AE004942 |
| 16 | 165.2 | 7.6 | 148068 | 1 | AB001488 |
| 17 | 165.2 | 7.6 | 209100 | 2 | BSUB0003 |
| 18 | 150.2 | 7.0 | 906 | 77 | CNS0104W |
| 19 | 147.8 | 6.8 | 316900 | 29 | TACID3 |
| 20 | 145.6 | 6.7 | 3116 | 2 | MSG1ACOX |
| 21 | 132.2 | 6.1 | 297762 | 71 | AC079853 |

Result 1 (16 hits)

| | | | | | | |
|----|-------|-----|--------|----|------------|---------------------|
| 22 | 107.4 | 5.0 | 259498 | 61 | AC020876 | Mus muscu |
| 23 | 104.8 | 4.9 | 731 | 77 | CNS01FEV | AL141752 Anopheles |
| 24 | 100.4 | 4.6 | 11886 | 1 | AE004638 | AE004638 Pseudomon |
| 25 | 94.8 | 4.4 | 110000 | 71 | AC078913_1 | Continuation (2 of |
| 26 | 87.6 | 4.1 | 41807 | 29 | SC6D11 | AE0158061 Streptomy |
| 27 | 84.6 | 3.9 | 16164 | 1 | AE004094 | AE004094 Vibrio ch |
| 28 | 72.6 | 3.4 | 1713 | 81 | A07753 | A07753 Recombinant |
| 29 | 71.8 | 3.3 | 15657 | 1 | AE001730 | AE001730 Thermotog |
| 30 | 69.8 | 3.2 | 96086 | 29 | STR5WMD1 | AF233324 Salmonell |
| 31 | 67.4 | 3.1 | 231916 | 73 | AL158037 | AL158037 Homo sapi |
| 32 | 66.4 | 3.1 | 146174 | 2 | D90910 | D90910 Synecocyst |
| 33 | 64.2 | 3.0 | 13725 | 1 | AE000832 | AE000832 Methanoba |
| 34 | 62.4 | 2.9 | 1788 | 1 | AF091510 | AF091510 Streptoco |
| 35 | 62.4 | 2.9 | 7045 | 2 | ECPPROM | X52659 E. coli tand |
| 36 | 62.4 | 2.9 | 7203 | 2 | EC01VGMED | M32253 E. coli 11v |
| 37 | 62.4 | 2.9 | 8088 | 2 | EC01VGMED | X04890 E. coli 11v |
| 38 | 62.4 | 2.9 | 14325 | 1 | AE000453 | AE000453 Escherich |
| 39 | 62.4 | 2.9 | 91414 | 2 | EC00W85 | M87049 E. coli gen |
| 40 | 60.8 | 2.8 | 2343 | 2 | EC01VX | V00290 E. coli gen |
| 41 | 60.8 | 2.8 | 2841 | 21 | E10718 | E10718 DNA encodin |
| 42 | 60.8 | 2.8 | 2841 | 81 | AR092608 | AR092608 Sequence |
| 43 | 60.8 | 2.8 | 2841 | 81 | E13058 | M37337 Escherichia |
| 44 | 60.8 | 2.8 | 4900 | 2 | EC00RN1V | M10313 E. coli 11v |
| 45 | 60.8 | 2.8 | 9456 | 2 | EC01VGE | |

ALIGNMENTS

RESULT 1

SC1A9 29400 bp DNA BCT 11-DEC-1998
 LOCATION Streptomyces coelicolor cosmid 1A9.
 ACCESSION AL034446
 VERSION AL034446.1 GI:4007685
 KEYWORDS

SOURCE

ORGANISM

Streptomyces coelicolor A3(2).
 Streptomyces coelicolor A3(2)
 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 Actinomycetales; Streptomycetaceae; Streptomyces.
 1 (bases 1 to 29400)
 Saunders, D.C. and Harris, D.
 Unpublished

REFERENCE

2 (bases 1 to 29400)
 Bentley, S.D., Parkhill, J., Barrell, B.G. and Rajandream, M.A.
 Direct Submission
 Submitted (04-DEC-1998) Streptomyces coelicolor sequencing project,
 Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge
 CB10 1SA E-mail: barrell@sanger.ac.uk Cosmids supplied by Prof.
 David A. Hopwood, [3] John Innes Centre, Norwich Research Park,
 Colney, Norwich, Norfolk NR4 7UH, UK

JOURNAL

3 (bases 1 to 29400)
 Redenbach, M., Kleiser, H.M., Denaplatte, D., Eichner, A., Cullum, J.,
 Kinashi, H. and Hopwood, D.A.
 A set of ordered cosmids and a detailed genetic and physical map
 for the 8 Mb Streptomyces coelicolor A3(2) chromosome
 Mol. Microbiol. 21 (1), 77-96 (1996)

TITLE

JOURNAL

MEDLINE

COMMENT

Notes:
 Streptomyces coelicolor sequencing at The Sanger Centre is funded
 by the BSRG.
 Details of S. coelicolor sequencing at the Sanger Centre are
 available on the World Wide Web.
 (URL: <http://www.sanger.ac.uk/Projects/S.coelicolor/>) CDS are
 numbered using the following system eg SC7B7.01c. SC (S.
 coelicolor), 7B7 (cosmid name), .01 (first CDS), c (complementary
 strand).

FEATURES

source

gene
 CDS

7

The more significant matches with motifs in the PROSITE database are also included but some of these may be fortuitous. The length in codons is given for each CDS.
 Usually the highest scoring match found by fasta -o is given for CDS which show significant similarity to other CDS in the database. The position of possible ribosome binding site sequences are given where these have been used to deduce the initiation codon. Gene prediction is based on positional base preference in codons using a specially developed Hidden Markov Model (Krogh et al., Nucleic Acids Research, 22(22):4768-4788(1994)) and the Frameplot program of Bibb et al., Gene 30:157-66(1984) as implemented at <http://www.nih.go.jp/jun/cgi-bin/frameplot.pl>. CAUTION: We may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, ggg, ttg or (act)) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream initiation codon.
 IMPORTANT: This sequence MAY NOT be the entire insert of the sequenced clone. It may be shorter because we only sequence overlapping sections once, or longer, because we arrange for a small overlap between neighbouring submissions. Cosmid 1A9 lies between 9B2 and 6C5 in the Ase-I-B genomic restriction fragment.
 Location/Qualifiers
 1..29400
 /organism="Streptomyces coelicolor A3(2)"
 /strain="A3(2)"
 /db_xref="taxon:100226"
 /clone="cosmid 1A9"
 /complement(1..651)
 /gene="SC1A9.01c"
 /complement(1..651)
 /gene="SC1A9.01c"
 /note="SC1A9.01c, incomplete CDS, possible transferase, partial CDS, len: 219 aa, similar to FR:053185 (EMBL:AL021246) a proposed transferase from Mycobacterium tuberculosis (302 aa), fasta scores: opt: 764, z-score: 1097.3, E(): 0, (62.1% identity in 203 aa overlap (302 aa). Also weakly similar to several methyltransferases eg. MEH_ECOLI (EMBL:X16584)5-methyltetrahydrofolate-homocysteine methyltransferase (1226 aa), fasta scores: opt:160, z-score: 234.8, E(): 8.4e-06, (30.0% identity in 220 aa overlap)."
 /codon_start=1
 /transl_table=11
 /product="putative transferase"
 /protein_id="CAA2371.1"
 /db_xref="GI:4007686"
 /translation="MTSDFADLASGGLVVDGGLSNLEAAGHLDALMSARLLADPEATIRRAHLAVFAGAEVATTSYVQAFEGFARCGIGREARALLSLVSAAREARRARRAPRAIRAVASAGPYAMLADSGEYRGKIGLGRGALERHFRLEVLARPDVLAIEVVDTEDEAALLRAVGLDVPALVSTYVAGDRRAGQIDFAALADADVEYI731..1634
 /gene="SC1A9.02"
 /note="SC1A9.02, possible transmembrane protein, len: 307aa; Contains several possible membrane spanning domains."
 /domain_start=1
 /codon_start=1
 /transl_table=11
 /product="putative transmembrane protein"
 /protein_id="CAA22372.1"
 /db_xref="GI:4007687"
 /translation="MTISGRIRTSVRCSPRHSHGDEGVPPVRFVQFLAVLVAVAGGIAVQVAKNDMDTLVLVGLTSVALVYFVAVMYRFREREDLVDLADGAARAGMTLIGFGLGAVTINLNFASGYEVDGIVGAGVGMMAAAATEEVEFGVYPRILEHICTGTAIGTGLVPGMLHNLNDATLTKALALATPAGMLAAATATNTMLTIGVHFGNNPAGGVSTFVSGNDSBLDATVSTSGPPLTIGDGFEGSVYSVGFVLLTLVFWLARRRNTVAFKGSRRRAAGANSATLPR1651..2817
 /gene="SC1A9.03"

CDS
 1651. 2817
 /gene="SCIA9.03"
 /note="SCIA9.03, probable two component sensor kinase, len: 388aa; similar to a family of sensor kinases egs. TR:Q53893 (EMBL:U51332) AbsA1 from Streptomyces coelicolor (571 aa), fasta scores: opt: 389, z-score: 278, E(): 2.9e-08, 33.1% identity in 405 aa overlap) and UPRK_ECOLI (EMBL:M17102) sensor kinase from Escherichia coli (500 aa), fasta scores: opt:221, z-score: 248.0, E(): 1.5e-06, (25.9% identity in 398 aa overlap). Contains several possible membrane spanning domains."
 /codon_start=1
 /transl_table=1
 /product="putative sensor kinase"
 /protein_id="CAA22373.1"
 /db_xref="gi:4007688"
 /translation="MIDRRVLELMRRLDVTPRDLPLGLVLLASLPSLGGSTETIGGLIPNRDLGVAVALQSIPIAVARRWTLILTLVSGFALSDOLRAVHIFAGALGICLVINAGSDQEKRRATQVATPLGYVAAVAGLNARGDTELYEVTFLVYLLANGICNWMRSRAAEERKSVAEDARNNAERTRIARLHHOVTHVTHVAVVQSAARYLAAPEBLDESLEAVSOTGRNALVDLNLHLLDLPMDIPDEPRPPRGVLTVEQVRRAGQPEETFEETGPAATSGSDLVAVRVOELNALTKYHGSTVSLVRHGEETIIVEGTGSGSCAASPGGSGRGLAGERNDVLGGESTDRPADGFFVARRIPGSGSGTA"
 2814. 3473
 /gene="SCIA9.04"
 2814. 3473
 /gene="SCIA9.04"
 /note="SCIA9.04, probable luxR family response regulator, len: 219 aa; similar to a family of regulators egs. TR:Q569816 (EMBL:AL023496) Probable two component regulator from Streptomyces coelicolor (224 aa) fasta scores: opt:714, z-score:1103.5, E():0. (54.8% identity in 219 aa overlap) and NARL_ECOLI (EMBL:X13360) nitrate/nitrite response regulator from Escherichia coli (216 aa) fasta scores: opt: 465, z-score: 656.5, E(): 2.7e-29, (37.6% identity in 213 aa overlap). Contains Pfam match to entry PF00072 response_reg, Response regulator-receiver domain, score 111.10, E-value 2.1e-29, Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20, PS00622 Bacterial regulatory proteins, luxR family signature and an helix-turn-helix motif from: 1 to: 219, score 983 (+2.53 SD)."
 /codon_start=1
 /transl_table=1
 /product="putative response regulator"
 /protein_id="CAA22374.1"
 /db_xref="gi:4007689"
 /translation="MSAIRVVICDDALITGATLVDAQPLEVEGCCDGTQVDA LARELRPVVAMDIEMPVGLDELTRRLAGGVAAHPKVLVLTFFNLDEYVYALRAGASCFGLINADPPDRLLHGIRIVAMGAAILLDPVTRRLVCRVARRIRPEGTRADIPLPRTETRETLRGLDLSNSEIFAVALVISPETVKTFVSRITLKLDRDQVAVVPRHGLV T"
 2826. 3173
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00072 response_reg, Response regulator receiver domain, score 111.10, E-value 2.1e-29"
 3276. 3470
 /gene="SCIA9.04"
 /note="Pfam match to entry PF00196 GERE, Bacterial regulatory proteins, luxR family, score 79.50, E-value 7e-20"
 3327. 3410
 /gene="SCIA9.04"
 /note="PS00622 Bacterial regulatory proteins, luxR family signature."
 complement(3492. 4094)
 /gene="SCIA9.05C"
 complement(3492. 4094)
 /gene="SCIA9.05C"
 /note="SCIA9.05C, possible bacterial transmembrane protein, len: 200 aa; contains possible membrane spanning hydrophobic regions"
 /codon_start=1

[illegible]

Db 539 TTCCGGCAATGTAGTCTATTGCGAGCTGTTCACAGCCCGAGCGATCCCAACAAGTA 538
 Qy 744 tgcatacagcgaatcagtcacacagcgcggaagcgtgctgcgtgagcagcagcagcagc 803
 Db 599 CTGGCGATTGCGATGCGCAAGGCGGCTTAACCGTGCGCTTTCGCTGTCGATTACCA 658
 Qy 804 gctgatacgcataagagaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 863
 Db 659 GCGGACCTGCGCTTAAACCTCGCCAGCAAGGGGCG--AAACCATGCACTGATCATGCGC 715
 Qy 864 ggcacccctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 923
 Db 716 CCACAAACCACTGCTGACGCGCGAGAAAGAAAGATTACGCAAACTGGGCGCACTGCTGCT 775
 Qy 924 aacgataagcctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 983
 Db 776 TATTCCAGCAATATCGCCCTGATGTGGCAGCGGCGCGCGCGCGCGCGCGCGCGCGCG 835
 Qy 984 tggagatcgagcaggaagaatlaaatacagcagcagcagcagcagcagcagcagcagcag 1043
 Db 836 GTTGGATTTCCTCGGAAATTAAGCGCCCTATTGTTTCATCCCTCCCGCTTAAGAAACAT 895
 Qy 1044 atcagcagatgagaatcgcgttggagcagcagcagcagcagcagcagcagcagcagcag 1103
 Db 896 GTTGAATACGATTAATCCGATGATGATTGATGATGATGATGATGATGATGATGATGAT 955
 Qy 1104 gtcgagcgtcgaatcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1163
 Db 956 TTCCGATACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1015
 Qy 1164 gattcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcctcct 1220
 Db 1016 GCTTTCATCCCGACCGACCATGCAAAATCATTCAGATTGATTCACCAACCGCACCATCG 1075
 Qy 1221 cgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1280
 Db 1076 GCTCAGCAGCAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1135
 Qy 1281 tgcgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1340
 Db 1136 CTTCGATTTGCTGAGAGAAAAGCGCATTCGCAATTTCTGATTAAGCGCTGGAAGATTAC 1195
 Qy 1341 gacgctaaagtcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1400
 Db 1196 CGCGACCGCCCGCAAGGCGCTGACGATTAAGTAAACCGCAGCG-----AGAAAGCG 1246
 Qy 1401 atcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1460
 Db 1247 ATTACCCCGCATATATCTGGCGCAGCAAAATTAATTCCTCCCGCATGACGCTATTTTC 1306
 Qy 1461 actgctgatacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1520
 Db 1307 ACTGATGAGGTTGATGAGCGCAAGGCTGGCGGCGCGCGCGCGCGCGCGCGCGCGCG 1363
 Qy 1521 agcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1580
 Db 1364 AACCGCTCGCGCTTACGTTTCCTTAACCAAGCTTTCGATGCTTAACCAAGCTTTCGATG 1423
 Qy 1581 atcgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1640
 Db 1424 CTGGGTCGCGAGCGCAGAGCGCAAGCGCATGCTGCTGCGCGCGCGCGCGCGCGCGCG 1483
 Qy 1641 tggagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1700
 Db 1484 TTTAGCATGTGATGAGCGCATTTCTCTCAGTATGATGATGATGATGATGATGATGATG 1343
 Qy 1701 gtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1760
 Db 1544 GTTCGCTTAAACCAAGCGCTGCTGCGCTTTCGATGATGATGATGATGATGATGATGATG 1603
 Qy 1761 cagagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1820

Db 1604 TTGACTACGCGCACCGCACTACAGACAAACTTTCGCCGATTCGCCAAGCGTGGCGC 1663
 Qy 1821 atcaaatcgcgtacgcatcacacagcagcagcagcagcagcagcagcagcagcagcagcagc 1880
 Db 1664 ATTACGGGTATCCGCTGTAGAAAAGCGTTCGATGATGATGATGATGATGATGATGATG 1723
 Qy 1881 gcatatcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1940
 Db 1724 TCCATGACCGCTCGCGGTGTGTGATGATGATGATGATGATGATGATGATGATGATG 1783
 Qy 1941 ccaacacacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2000
 Db 1784 CCGCAGATCAAACTCGACAGCGCAAGGTTTCAGCTGATATGCTGCTGCGCAATCATC 1843
 Qy 2001 gtcgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 2042
 Db 1844 AGCGAGCGCGGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1885

RESULT 3
 AE000188/c
 LOCUS
 DEFINITION
 accession
 version
 keywords
 source
 organism
 Escherichia coli.
 Escherichia coli.
 Escherichia coli.
 Bacteria: Proteobacteria: gamma subdivision: Enterobacteriaceae:

REFERENCE
 AUTHORS
 1 (bases 1 to 11429)
 Blattner, F.R., Plunkett, G. III, Bloch, C.A., Perna, N.T., Burland, V.,
 Riley, M., Collado-Vides, J., Glasner, J.D., Rode, C.K., Mayhew, G.F.,
 Gregor, J., Davis, N.W., Kirkpatrick, H.A., Goeden, M.A., Rose, D.J.,
 Mau, B. and Shao, Y.
 The complete genome sequence of *Escherichia coli* K-12
 Science 277 (5331), 1453-1474 (1997)

REFERENCE
 AUTHORS
 2 (bases 1 to 11429)
 Blattner, F.R.
 Direct Submission
 Submitted (16-JAN-1997) Guy Plunkett III, Laboratory of Genetics,
 University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
 Email: ecoligenetics.wisc.edu Phone: 608-262-2534 Fax:
 608-263-7459

REFERENCE
 AUTHORS
 3 (bases 1 to 11429)
 Blattner, F.R.
 Direct Submission
 Submitted (02-SEP-1997) Guy Plunkett III, Laboratory of Genetics,
 University of Wisconsin, 445 Henry Mall, Madison, WI 53706, USA.
 Email: ecoligenetics.wisc.edu Phone: 608-262-2534 Fax:
 608-263-7459

REFERENCE
 AUTHORS
 4 (bases 1 to 11429)
 Plunkett, G. III.
 Direct Submission
 Submitted (13-OCT-1998) Laboratory of Genetics, University of
 Wisconsin, 445 Henry Mall, Madison, WI 53706, USA

COMMENT
 This sequence was determined by the E. coli Genome Project at the
 University of Wisconsin-Madison (Frederick R. Blattner, director).
 Supported by NIH grants HG00301 and HG01428 (from the Human Genome
 Project and NCHGR). The entire sequence was independently
 determined from E. coli K-12 strain MG1655. Predicted open reading
 frames were determined using Genemark software, kindly supplied by
 Mark Borodovsky, Georgia Institute of Technology, Atlanta, GA.
 30332 [e-mail: mark@ember.gatech.edu]. Open reading frames that
 have been correlated with genetic loci are being annotated with CG
 site Nos., unique ID nos. for the genes in the E. coli Genetic
 Stock Center (CGSC) database at Yale University, kindly supplied by
 Mary Berlyn. A public version of the database is accessible
 (http://cgsc.biology.yale.edu). Annotation of the genome is an
 ongoing task whose goal is to make the genome sequence more useful

Ikemoto,K., Inada,T., Isono,K., Isono,S., Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S., Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nishimoto,H., Nishio,Y., Oshima,T., Saito,N., Sempel,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,K. and Yano,M.

The systematic sequencing of the *Escherichia coli* genome in Japan unpublished (1996)

3 (sites)

Oshima,T., Alba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Ikemoto,K., Inada,T., Itoh,T., Kajihara,M., Kanai,K., Kashimoto,K., Kimura,S., Kitagawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nishimoto,H., Nishio,Y., Saito,N., Sempel,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y., Yano,M. and Yano,M.

A 718-kb DNA sequence of the *Escherichia coli* K-12 genome corresponding to the 12.7-28.0 min region on the linkage map DNA Res. 3 (3), 137-155 (1996)

Collaboration Information:

Project:

The Japan E. coli genome DNA sequencing project

Group:

The Japan E. coli genome DNA sequencing group

Members: (1995.4 - 1996.3)

Alba,H., Baba,T., Fujita,K., Hayashi,K., Honjo,A., Horuchi,T., Ikemoto,K., Inada,T., Isono,K., Isono,S., Itoh,T., Kanai,K., Kasai,H., Kashimoto,K., Kim,S., Kimura,S., Kitagawa,M., Kitakawa,M., Makino,K., Masuda,S., Miki,T., Mizobuchi,K., Mori,H., Motomura,K., Nakamura,Y., Nishimoto,H., Nishio,Y., Oshima,T., Saito,N., Sempel,G., Seki,Y., Tagami,H., Takemoto,K., Wada,C., Yamamoto,Y. and Yano,M.

Headed by:

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URL:

The Japan E. coli genome database

http://sw3.aist-nara.ac.jp

FEATURES

source

1. 19978

/organism="Escherichia coli"

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 VERSION L47688.1 GI:1009026
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SOURCE oxidase.
 ORGANISM Escherichia coli (individual isolate mutant poxb10, strain K-12)
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Escherichia coli
 REFERENCE 1 (bases 1 to 1719)
 AUTHORS Grabau, C., Chang, Y.-Y. and Cronan, J.E., Jr.
 TITLE Lipid binding by Escherichia coli pyruvate oxidase is disrupted by
 small alterations of the carboxyl-terminal region
 JOURNAL J. Biol. Chem. 264 (21), 12510-12519 (1989)
 MEDLINE 89308683
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 SOURCE Escherichia coli (strain K-12) DNA.
 ORGANISM Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Escherichia.
 REFERENCE 1 (bases 1 to 1719)
 AUTHORS Grabau,C., Chang,Y.Y. and Cronan,J.E. Jr.
 TITLE Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small alterations of the carboxyl-terminal region
 JOURNAL J. Biol. Chem. 264 (21), 12510-12519 (1989)
 MEDLINE 89308683
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 REFERENCE 1 (bases 1 to 1719)
 AUTHORS Grabau, C., Chang, X.Y. and Cronan, J.E. Jr.
 TITLE Lipid binding by Escherichia coli pyruvate oxidase is disrupted by
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 JOURNAL J. Biol. Chem. 264 (21), 12510-12519 (1989)
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| TITLE | Grabau, C., Chang, Y. Y. and Cronan, J. E. Jr. | | |
| JOURNAL | Lipid binding by Escherichia coli pyruvate oxidase is disrupted by small alterations of the carboxyl-terminal region | | |
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 ORGANISM Pseudomonas amyloclavata

REFERENCE Bacteria: Proteobacteria.
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AUTHORS Amemura, A.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1988) Amemura A., The Institute of Scientific and Industrial Research, Osaka University, 8-1 Mihogaoka, Ibaraki, Osaka 567, Japan
2 (bases 1 to 1440)
Amemura, A., Fujita, M. and Futai, M.
JOURNAL Unpublished
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Pseudomonas.
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AUTHORS
Stover, C. K., Pham, X. Q., Erwin, A. L., Mizoguchi, S. D., Warrenner, P., Hickey, M. J., Brinkman, F. S., Hutnagle, W. O., Kowalik, D. J., Lagrou, M., Garber, R. L., Goltzy, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L. L., Coulter, S. N., Folger, K. R., Kas, A., Larbig, K., Lim, R., Smith, K., Spencer, D., Wong, G. K., Wu, Z. and Paulsen, I. T.
Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen
JOURNAL
Nature 406 (6799), 959-964 (2000)
MEDLINE
2 (bases 1 to 10977)
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AUTHORS
Stover, C. K., Pham, X. Q., Erwin, A. L., Mizoguchi, S. D., Warrenner, P., Hickey, M. J., Brinkman, F. S., Hutnagle, W. O., Kowalik, D. J., Lagrou, M., Garber, R. L., Goltzy, L., Tolentino, E., Westbrock-Wadman, S., Yuan, Y., Brody, L. L., Coulter, S. N., Folger, K. R., Kas, A., Larbig, K., Lim, R., Smith, K., Spencer, D., Wong, G. K., Wu, Z., Paulsen, I. T., Reizer, J., Salier, M. H., Hancock, R. E. W., Lory, S. and Olson, M. V.
Direct Submission
Submitted (16-May-2000) Department of Medicine and Genetics, University of Washington Genome Center, University Of Washington, Box 352145, Seattle, WA 98195, USA
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